

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:14:43 ; Search time 373.587 Seconds  
(Without alignments)  
10012.591 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661

Sequence: 1 GAATTCGGCTTCATATGCA.....TGGCGGATTAAGCCGATTC 1661

Scoring table: IDENTITY-NUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

N\_Geneseq\_101002:\*

1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
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10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
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21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1661	100.0	1661	20 AAX86155
2	1632.2	97.7	1635	24 AAB99100
3	1413.4	85.1	1683	22 AAB98861
4	1140.4	68.7	1306	22 AAB56862
5	1122.6	67.6	1305	22 AAB56865
6	1053.4	64.0	2155561	24 AAB71527
7	1052.4	64.0	1620	24 AAB69159
8	1052	63.3	1654	20 AAX86153
9	1039.2	62.6	1623	22 AAB90800

10	1038.4	62.5	1926	22 AAR25036
11	1037	62.4	2107	22 AAB56860
12	1036	62.4	1647	22 AAB90906
13	1035.4	62.3	5365	19 AAV52210
14	1030.6	62.0	2401	22 AAB56859
15	955	57.5	2165589	24 ABA90521
16	942.6	56.7	3625	20 AAX12979
17	832	50.1	1901	24 ABO70705
18	824	49.6	213251	24 ABO67193
19	786.4	47.3	1957	22 AAB56868
20	773	46.5	1958	22 AAB56867
21	760.6	45.8	1570	24 AAB069121
22	756.4	45.5	3885	22 AAB54519
23	755.4	45.5	1620	22 AAB52898
24	735.6	44.3	1623	24 AAB92405
25	722.4	43.5	2712	22 AAB56866
26	704.2	42.4	1647	18 AAR69201
27	704.2	42.4	4872	18 AAR69203
28	654.2	39.4	96109	22 AAR28348
29	613.8	37.1	640681	22 ABA92787
30	608.2	36.6	613	22 AAB56864
31	604.2	36.4	609	22 AAB56863
32	590.6	35.6	1665	20 AAX86152
33	589.8	35.5	1647	21 AAB48498
34	589.8	35.5	1647	22 AAC90805
35	589.8	35.5	1647	24 ABL96324
36	589.8	35.5	1741	22 AAB56858
37	589.8	35.5	2155	24 AAD33423
38	589.8	35.5	4524	21 AAB48500
39	583.4	35.1	2032	22 AAB56856
40	577.2	34.8	2006	22 AAB56857
41	568.2	34.2	1662	20 AAX86154
42	552.8	33.3	1635	21 AAY54509
43	551.6	33.2	910715	20 AAY20248
44	550	33.1	2465	12 AAI13136
45	536.8	32.3	1635	21 AAI13000

## ALIGNMENTS

RESULT 1	AAX86155
ID	AAX86155 standard; DNA: 1661 BP.
AC	AAX86155;
DT	22-SEP-1999 (first entry)
DE	DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.
XX	Heat shock protein: Hsp60-2; Immune response; Immunological carrier;
KW	Cancer control; tumour; sarcoma; cancer; gene therapy; ss.
OS	Streptococcus pyogenes.
XX	
XX	MO9935270-A1.
PD	15-JUL-1999.
XX	
XX	29-DEC-1998; 98MO-CA01203.
XX	
XX	31-DEC-1997; 97US-0001737.
XX	
XX	(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX	
XX	Mizzen L, Walslewski J;
XX	WPI; 1999-433937/36.
XX	P-PSDB: AAY23904.
XX	New nucleic acid encoding heat shock protein-60 from Streptococcus;
XX	useful in vaccines, as carriers for other immunogens, as anticancer

PT agents and for diagnosis

PS Claim 3: Fig 4A-B; 176bp; English.

XX The present sequence encodes a heat shock protein, designated Hsp60-2.  
 CC The protein, its fragments, variants and fusion proteins, are  
 CC used to elicit or enhance an immune response against Streptococcus,  
 CC and to elicit a similar response to a target antigen fused to the  
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not  
 CC immunosuppressive so provide an increased response to any conjugated or  
 CC fused antigen. Also, where used for cancer control, they lack the side  
 CC effects associated with endotoxins. They can also be used to detect  
 CC specific antibodies and in treatment or prevention of tumours  
 CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
 CC liver). The Hsp60 polynucleotide is used for recombinant production  
 CC of the protein, as a source of primers and probes for detecting  
 CC streptococci in standard hybridization/amplification assay, and  
 CC therapeutically in gene therapy vectors.

SQ Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other:

Query Match 100.0%; Score 1661; DB 20; Length 1661;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 GAATTCGGCTTCATATGCGAAGAAAGAAATTCGACGATGCGGCTGCTCCATG 60  
 DB 1 GAATTCGGCTTCATATGCGAAGAAAGAAATTCGACGATGCGGCTGCTCCATG 60  
 0Y 61 TCGGGGAGTTGATATGTTAGCAGATACGCTCAAGTAAAGCTTGTCCATAAGGCGCA 120  
 DB 61 TCGGGGAGTTGATATGTTAGCAGATACGCTCAAGTAAAGCTTGTCCATAAGGCGCA 120  
 0Y 121 ATGCTGTTCTTGAAGAAAGCTTTGGTTCTCCCTTAATTAATGACGGGTAACATTG 180  
 DB 121 ATGCTGTTCTTGAAGAAAGCTTTGGTTCTCCCTTAATTAATGACGGGTAACATTG 180  
 0Y 181 CTAAGAGATGATAGATAGATATTTGAAAGATGAGGCAAAATTTGGTGTCAAG 240  
 DB 181 CTAAGAGATGATAGATAGATATTTGAAAGATGAGGCAAAATTTGGTGTCAAG 240  
 0Y 241 TGGCTCTTAAGCAATGATATGCTGTATGAGGACACACTGCAAGCTTTGACAC 300  
 DB 241 TGGCTCTTAAGCAATGATATGCTGTATGAGGACACACTGCAAGCTTTGACAC 300  
 0Y 301 AAGCCATTTGTCATGAAAGAGCTAAAGAAATGAGCAGAGCTGTAATCCATTTGTC 360  
 DB 301 AAGCCATTTGTCATGAAAGAGCTAAAGAAATGAGCAGAGCTGTAATCCATTTGTC 360  
 0Y 361 GTGAGGATTTGAAGACAGACAGACAGCTGTTGAAGCCCTTGAAGCCATTTGTCAC 420  
 DB 361 GTGAGGATTTGAAGACAGACAGACAGCTGTTGAAGCCCTTGAAGCCATTTGTCAC 420  
 0Y 421 CTGTATCTGGCAGAGAGCTATGCTGAGTGCAGATATCATGAGCTCTGAAAAAG 480  
 DB 421 CTGTATCTGGCAGAGAGCTATGCTGAGTGCAGATATCATGAGCTCTGAAAAAG 480  
 0Y 481 TTGAGAGATATATCTGAGAGCTATGAGAGCTGTGGGACAGATGATATCAATG 540  
 DB 481 TTGAGAGATATATCTGAGAGCTATGAGAGCTGTGGGACAGATGATATCAATG 540  
 0Y 541 AAGATCTCGAGGATGAGAAAGAACTGTAAGTGTGAAGGACATGCAATTTACCGTG 600  
 DB 541 AAGATCTCGAGGATGAGAAAGAACTGTAAGTGTGAAGGACATGCAATTTACCGTG 600  
 0Y 601 GTTACCTGCTCAATACATGTCACACACATGAAAAATGTTGACAGCTTGAAGACC 660  
 DB 601 GTTACCTGCTCAATACATGTCACACACATGAAAAATGTTGACAGCTTGAAGACC 660  
 0Y 661 CATTTATCTTAACCGGATAAAAAGTCAACATCAAGACATTTTGGCACTACTTG 720  
 DB 661 CATTTATCTTAACCGGATAAAAAGTCAACATCAAGACATTTTGGCACTACTTG 720

0Y 721 AGCAAGTTCTTAACCAACACCGTCCATTAATTCAGATGATGATGATGAG 780  
 DB 721 AGCAAGTTCTTAACCAACACCGTCCATTAATTCAGATGATGATGATGATGAG 780  
 0Y 781 CACTTCCAAACCTTGTCTTGAACAGATTCGTGACTTTCATATGTTGCTGTCAAG 840  
 DB 781 CACTTCCAAACCTTGTCTTGAACAGATTCGTGACTTTCATATGTTGCTGTCAAG 840  
 0Y 841 CGCCAGATTTGTGATGCTGCTGAAGAGTATGCTGAACACATGCTATCTGACAGTG 900  
 DB 841 CGCCAGATTTGTGATGCTGCTGAAGAGTATGCTGAACACATGCTATCTGACAGTG 900  
 0Y 901 GTACAGATTTGACAGATCTGAGACTTGAATTAAGATGCTACATGACAGCCCTG 960  
 DB 901 GTACAGATTTGACAGATCTGAGACTTGAATTAAGATGCTACATGACAGCCCTG 960  
 0Y 961 GACAGGCTCTAAGATTAAGTGAATGAATGACAGATATTTGTAAGGTGACGAA 1020  
 DB 961 GACAGGCTCTAAGATTAAGTGAATGAATGACAGATATTTGTAAGGTGACGAA 1020  
 0Y 1021 GTTCAGAGCTATGCTTAACCGTATTCGATGATTAATCGCATTTGAACACACTT 1080  
 DB 1021 GTTCAGAGCTATGCTTAACCGTATTCGATGATTAATCGCATTTGAACACACTT 1080  
 0Y 1081 CTGACTTTACCGTGAAGAAATCTAAGAAAGCTTTGGCGAAATTAAGCTGTGTAGCTG 1140  
 DB 1081 CTGACTTTACCGTGAAGAAATCTAAGAAAGCTTTGGCGAAATTAAGCTGTGTAGCTG 1140  
 0Y 1141 TTATCAAGTAGAGCTCCACAGAGACAGCTTTAAAGAAATGAACTTCGATTGAG 1200  
 DB 1141 TTATCAAGTAGAGCTCCACAGAGACAGCTTTAAAGAAATGAACTTCGATTGAG 1200  
 0Y 1201 ATGCTTAATGCTACAGCTGACGCGCTTGAAGAGTATCGTTGCTGGTGTGAGACAG 1260  
 DB 1201 ATGCTTAATGCTACAGCTGACGCGCTTGAAGAGTATCGTTGCTGGTGTGAGACAG 1260  
 0Y 1261 CACTTAATGCTTATTAAGAAAGATGACAGCTTGAAGTGAAGGAGATGATGCTACTG 1320  
 DB 1261 CACTTAATGCTTATTAAGAAAGATGACAGCTTGAAGTGAAGGAGATGATGCTACTG 1320  
 0Y 1321 GAGGTACAGTGTGCTGCTGCTGCTGCTGAAGAGCTGTAAGTGAAGTGAAGTGAAG 1380  
 DB 1321 GAGGTACAGTGTGCTGCTGCTGCTGCTGAAGAGCTGTAAGTGAAGTGAAGTGAAG 1380  
 0Y 1381 GGTACAGAGCTCCGTTGATTAAGCAAGTTGAAGAAAGCCCTGACAGACAGATTTA 1440  
 DB 1381 GGTACAGAGCTCCGTTGATTAAGCAAGTTGAAGAAAGCCCTGACAGACAGATTTA 1440  
 0Y 1441 ATGCTCAACAGGTGAGTGGTGAATGATTAAGCAAGATGATGACCTGTCAAG 1500  
 DB 1441 ATGCTCAACAGGTGAGTGGTGAATGATTAAGCAAGATGATGACCTGTCAAG 1500  
 0Y 1501 TAACAGATCAGCGCTTCAAAATGACAGCTTCTAGCTAGTCTTAATTTGACACAGAG 1560  
 DB 1501 TAACAGATCAGCGCTTCAAAATGACAGCTTCTAGCTAGTCTTAATTTGACACAGAG 1560  
 0Y 1561 CAGTTGTTGCTAATAACCTGAACAGAGCTGACAGCTGACAGCAATGCGAGGTATGG 1620  
 DB 1561 CAGTTGTTGCTAATAACCTGAACAGAGCTGACAGCTGACAGCAATGCGAGGTATGG 1620  
 0Y 1621 ATCCAGATGATGCTGGATGAGGAGGATTAAGCCGAATTC 1661  
 DB 1621 ATCCAGATGATGCTGGATGAGGAGGATTAAGCCGAATTC 1661

RESULT 2  
 ABN69160  
 ID ABN69160 standard; DNA: 1635 BP.  
 XX ABN69160;  
 AC  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX

DE Streptococcus polynucleotide SEQ ID NO 6233.  
XX  
KW Streptococcus: GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.  
OS Streptococcus pyogenes.  
XX  
FN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB04789.  
XX  
PR 27-OCT-2000; 2000GB-0026333.  
PR 24-NOV-2000; 2000GB-0028727.  
PR 07-MAR-2001; 2001GB-0005640.  
XX  
PA (CHIR-) CHIRON SPA.  
XX (GENO-) INST GENOMIC RES.  
PI Telford J, Maignan V, Margalit Ros YI, Grandi G, Fraser C;  
PI Tellelin H;  
XX WPI: 2002-352536/38.  
DR P-PSDB; ABP28529.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection  
or disease caused by Streptococcus bacteria, such as meningitis, and  
for detecting a compound that binds to the protein -  
XX  
PS Claim 7; Page 3785-3786; 4525pp; English.  
XX  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
the specification. The proteins have antibacterial and antiinflammatory  
activity. (I), nucleic acids encoding (II), ABN6044-ABN7156 and  
antibodies that bind (I) are used in the manufacture of medicaments for  
the treatment or prevention of infection or disease caused by  
Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
biological sample. (I) is used to determine whether a compound binds to  
CC (II). A composition comprising (I) or a nucleic acid encoding (I), may be  
used as a vaccine or diagnostic composition. The disease caused by  
Streptococcus that is prevented or treated may be meningitis. Nucleic  
acid encoding (I) may be used to recombinantly produce (I) and may be  
used in gene therapy. Antibodies to (I) are used for affinity  
chromatography, immunoassays, and distinguishing/identifying  
Streptococcus proteins.  
XX  
XX Sequence 1635 BP; 504 A; 303 C; 397 G; 431 T; 0 other;  
SO  
Query Match 97.7%; Score 1622.2; DB 24; Length 1635;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 253 CCAATGATATTCCTGCTGATGGAGAGACTACGCAAGATTGACACAGCAATGCTTC 312  
DB CCAATGATATTCCTGCTGATGGAGAGACTACGCAAGATTGACACAGCAATGCTTC 304  
QY 313 ATGAGAGACTAAAAATGTGACAGCAGGTGTCAATGATGATGATGATGATGATGATG 372  
DB ATGAGAGACTAAAAATGTGACAGCAGGTGTCAATGATGATGATGATGATGATGATG 364  
QY 373 AACAGCAGCAGCAAGCCTGTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 432  
DB AACAGCAGCAGCAAGCCTGTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 424  
QY 433 AGGAGCTATTTGCTGAGGTGCTGAGATATCAGCTTGAAGCTTGAAGCTTGAAGCTTGA 492  
DB AGGAGCTATTTGCTGAGGTGCTGAGATATCAGCTTGAAGCTTGAAGCTTGAAGCTTGA 484  
QY 493 TCTCAGAGCTATGAGCCTGTGGGCAACAGATGATGATGATGATGATGATGATGATG 552  
DB TCTCAGAGCTATGAGCCTGTGGGCAACAGATGATGATGATGATGATGATGATGATG 544  
QY 553 GTATGGAACAGAACTTGAAGGTGTTGAAGCATATTTGACCGGTGCTGCTGCTGCTGCTG 612  
DB GTATGGAACAGAACTTGAAGGTGTTGAAGCATATTTGACCGGTGCTGCTGCTGCTGCTG 604  
QY 613 AATACATGCTCAGACATGAAATATGCTGACAGCTTGAAGCTTGAAGCTTGAAGCTTGA 672  
DB AATACATGCTCAGACATGAAATATGCTGACAGCTTGAAGCTTGAAGCTTGAAGCTTGA 664  
QY 673 TCACGATATTAAGGTGCTCAACATCCACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 732  
DB TCACGATATTAAGGTGCTCAACATCCACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 724  
QY 733 AAACACCCCTCCTTACATATTTGACATGATGATGATGATGATGATGATGATGATGATG 792  
DB AAACACCCCTCCTTACATATTTGACATGATGATGATGATGATGATGATGATGATGATG 784  
QY 793 TTCTCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 852  
DB TTCTCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 844  
QY 853 GTGATGCTGCTGAAGCATGCTTGAAGCATGCTTGAAGCATGCTTGAAGCATGCTTGA 912  
DB GTGATGCTGCTGAAGCATGCTTGAAGCATGCTTGAAGCATGCTTGAAGCATGCTTGA 904  
QY 913 CAGAGATCTAGCATGCTTGAAGCATGCTTGAAGCATGCTTGAAGCATGCTTGAAGCATG 972  
DB CAGAGATCTAGCATGCTTGAAGCATGCTTGAAGCATGCTTGAAGCATGCTTGAAGCATG 964  
QY 973 AGATTAAGCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1032  
DB AGATTAAGCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1024  
QY 1033 TTGCTTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1092  
DB TTGCTTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1084  
QY 1093 GTGAAAACTGACAGAGCTTGGCGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1152  
DB GTGAAAACTGACAGAGCTTGGCGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144  
QY 1153 GAGCTCCAGAGAGAGAGCTTGAAGCAATGATGATGATGATGATGATGATGATGATG 1212  
DB GAGCTCCAGAGAGAGAGCTTGAAGCAATGATGATGATGATGATGATGATGATGATG 1204  
QY 1213 CTACAGCGAGAGCGCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATG 1272  
DB CTACAGCGAGAGCGCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATG 1264  
QY 1273 TTATGAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1332  
DB TTATGAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1324  
QY 1333 TGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1392

Db 1325 TGCCTTCCTCTAGACAGCCCTGTAACGTAATGCTTTAAAGCTGGGTACGAGGCT 1384  
 OY 1339 CCGAGCTTTTTCACAGTTTAAACACCCCTGACGAAACAGATTTATGCTGCACAG 1452  
 Db 1385 CCGAGCTTTTTCACAGTTTAAACACCCCTGACGAAACAGATTTATGCTGCACAG 1444  
 OY 1433 GTGAGTGGTGTATGATTTAAACAGGATCATTGACCCCTGTCGTAAGTACAGCATG 1512  
 Db 1445 GTGAGTGGTGTATGATTTAAACAGGATCATTGACCCCTGTCGTAAGTACAGCATG 1504  
 OY 1513 CGCTTCAAAATGACAGCTTGTAGTACTCTTATTTTGAACAAGACAGTGTGTGCTA 1572  
 Db 1505 CGCTTCAAAATGACAGCTTGTAGTACTCTTATTTTGAACAAGACAGTGTGTGCTA 1564  
 OY 1573 ATAACTCAACAGCTACGCGCAGGAGCAGATGCGACAGATGATGATGATGATGATG 1632  
 Db 1565 ATAACTCAACAGCTACGCGCAGGAGCAGATGCGACAGATGATGATGATGATGATG 1624  
 OY 1633 TGGGTGG 1639  
 Db 1625 TGGGTGG 1631  
 RESULT 3  
 AAH56861  
 ID AAH56861 standard; DNA: 2683 BP.  
 XX  
 AC AAH56861:  
 XX  
 DT 06-SEP-2001 (first entry)  
 DE  
 XX S. Pyogenes groEL gene partial sequence SEQ ID NO:7.  
 XX  
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;  
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;  
 KW Streptococcus pyogenes; Streptococcus aureus; Pseudomonas aeruginosa;  
 KW antibacterial; antiviral; antiproliferative; antisense therapy;  
 KW microbial infection; ds.  
 XX  
 OS Streptococcus pyogenes.  
 XX  
 PN WO200136625-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 20-NOV-2000; 2000WO-CN01347.  
 XX  
 PR 18-NOV-1999; 99US-0166249.  
 XX  
 PA (GENE-) GENESENSE TECHNOLOGIES INC.  
 XX  
 PI Wright JA, Young AH, Dugourd D;  
 XX  
 DR WPI; 2001-355633/37.  
 XX  
 PT Novel antisense compounds targeting nucleic acid encoding groEL or  
 PT groES gene of microorganism, which hybridize with and inhibit  
 PT expression of the genes, useful to inhibit growth of microorganism  
 PT having the genes.  
 XX  
 PS Disclosure: Fig 7; 110pp: English.  
 CC  
 CC The present invention specifically claims AAH56368 to AAH56832 which are  
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More  
 CC generally, antisense compounds (I) comprising antisense oligonucleotides  
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat  
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a  
 CC microorganism, where the antisense compound is complementary to GL or  
 CC GS of a microorganism and specifically hybridizes with and inhibits the  
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral  
 CC and antiproliferative activities, and can be used in antisense therapy  
 CC and for inhibition of expression of groES or groEL. (I) are useful for

CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are  
 CC also useful for inhibiting the growth of a microorganism, or inhibiting  
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or  
 CC a virus) having a GL or GS gene which involves administering to the  
 CC microorganism or to a cell infected with the microorganism, (I). (I) are  
 CC also useful for treating a mammalian pathological condition mediated by  
 CC the microorganisms which involves identifying a eukaryotic organism having a GL  
 CC or GS gene and administering (I) such that the growth of microorganism  
 CC is inhibited. The antisense compounds are utilized for diagnostics, to  
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
 CC prevent or delay microbial infections in humans. They are also useful as  
 CC molecular weight markers. AAH56368 to AAH56367 and AAH56832 to AAH56834  
 CC represent PCR primers for groE sequences which are used in the  
 CC exemplification of the present invention. AAH56855 to AAH56870 represent  
 CC groE nucleotide sequence given in the present invention.  
 XX  
 XX Sequence 2683 BP; 808 A; 490 C; 593 G; 792 T; 0 other;  
 Query Match 85.1%; Score 1413.4; DB 22; Length 2683;  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 1423; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 OY 201 GATCATTTTGAACATGGAGCAGCAAAATGGTGTGATGAGTGGCTTCAAAACCATGAT 260  
 Db 1 GATCATTTTGAACATGGAGCAGCAAAATGGTGTGATGAGTGGCTTCAAAACCATGAT 60  
 OY 261 ATTGCTGTGATGGAGCAGCTACTGCAACAGTTTGCACAAAGCATTTGTCATAGAGA 320  
 Db 61 ATTGCTGTGATGGAGCAGCTACTGCAACAGTTTGCACAAAGCATTTGTCATAGAGA 120  
 OY 321 CTAAAAATGTGACAGCAGTGTCTAATCCAAATGTGTATCCGTGAGCATTTGAACAGCA 380  
 Db 121 CTAAAAATGTGACAGCAGTGTCTAATCCAAATGTGTATCCGTGAGCATTTGAACAGCA 180  
 OY 381 ACAGCAACAGCTGTGAAAGCTTGAAGGCAATTGCTCACTGATTCGCAAGAGAGCT 440  
 Db 181 ACAGCAACAGCTGTGAAAGCTTGAAGGCAATTGCTCACTGATTCGCAAGAGAGCT 240  
 OY 441 ATTGCTGTGATGGAGCAGCTACTGCAACAGTTTGCACAAAGCATTTGTCATAGAGA 500  
 Db 241 ATTGCTGTGATGGAGCAGCTACTGCAACAGTTTGCACAAAGCATTTGTCATAGAGA 300  
 OY 501 GCTATGGAGCTGTGGGCAACGATGATGATACATGAGTGTGATGATGATGATGATGATG 560  
 Db 301 GCTATGGAGCTGTGGGCAACGATGATGATACATGAGTGTGATGATGATGATGATGATG 360  
 OY 561 ACAGCACTGAGTGTGAAAGCAGCAATTTGACCGTGTACCTGCTCAATACATG 620  
 Db 361 ACAGCACTGAGTGTGAAAGCAGCAATTTGACCGTGTACCTGCTCAATACATG 420  
 OY 621 GTCACAGCAATGAAAAATGTTGACAGCTTGAAGACCTTGAAGAGTCTTAAACCAAC 680  
 Db 421 GTCACAGCAATGAAAAATGTTGACAGCTTGAAGACCTTGAAGAGTCTTAAACCAAC 480  
 OY 681 AAAAAGTGTCAACATCCAGACATTTTGGCACTAGCTGAGAGTCTTAAACCAAC 740  
 Db 481 AAAAAGTGTCAACATCCAGACATTTTGGCACTAGCTGAGAGTCTTAAACCAAC 540  
 OY 741 CGTCCATTACTATTATTCAGATGATGATGATGATGATGATGATGATGATGATGATG 800  
 Db 541 CGTCCATTACTATTATTCAGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 OY 801 AACCAATTCGTGAGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 860  
 Db 601 AACCAATTCGTGAGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 660  
 OY 861 CGTAAAGCTATGCTGAGCAATGCTATGCTGACAGCTGACAGCTGACAGCTGACAGCT 920  
 Db 661 CGTAAAGCTATGCTGAGCAATGCTATGCTGACAGCTGACAGCTGACAGCTGACAGCT 720  
 OY 921 CTGAGCTGATTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 980  
 Db 721 CTGAGCTGATTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 980

Db 721 CTAGACTTGAATTAAGATGCTACATGACACCCCTTGAGACGGCTGCTAAGATTACA 780  
 Qy 981 GTTGATTAAGATGACAGATTAATGTTGAAGTTCAGAGATTACAGACTATTGTAAC 1040  
 Db 781 GTTGATTAAGATGACAGATTAATGTTGAAGTTCAGAGATTACAGACTATTGTAAC 840  
 Qy 1041 CGATTGCTGATTAATTCGCAATTAGAAACACAACTTCTGACTTTGACCGTGAATAA 1100  
 Db 841 CGATTGCTGATTAATTCGCAATTAGAAACACAACTTCTGACTTTGACCGTGAATAA 900  
 Qy 1101 CTACAGACGTTGGCAAAATAGTGTGCTGATGCTGTATCAAAAGTAGAGCTCCA 1160  
 Db 901 CTACAGACGTTGGCGAAATAGTGTGCTGATGCTGTATCAAAAGTAGAGCTCCA 960  
 Qy 1161 ACAGAGACGCTTTAAAGAAATGAAACTTGCAATGAGATGCTCTTAAGCTACACGT 1220  
 Db 961 ACAGAGACGCTTTAAAGAAATGAAACTTGCAATGAGATGCTCTTAAGCTACACGT 1020  
 Qy 1221 GGAGCGCTGAAGAGATTAAGTGTGCTGCTGCTGGAACACACTTATTACGTTATTGA 1280  
 Db 1021 GGAGCGCTGAAGAGATTAAGTGTGCTGCTGCTGGAACACACTTATTACGTTATTGA 1080  
 Qy 1281 AATGACAGCTCTTGACCTTGAGGGCGATGATGCTACTGAGACGATACACTTGTCTTCT 1340  
 Db 1081 AATGACAGCTCTTGACCTTGAGGGCGATGATGCTACTGAGACGATACACTTGTCTTCT 1140  
 Qy 1341 GCTCTAGAAAGCTGTACGTCAATTTGCTTTAATGCTGGTAGAGAGCTCCGTAGTT 1400  
 Db 1141 GCTCTAGAAAGCTGTACGTCAATTTGCTTTAATGCTGGTAGAGAGCTCCGTAGTT 1200  
 Qy 1401 ATGACAAAGTTGAAAAACAGCCCTGCAGAGACAGAGATTATGCTGCAACAGGTGAGTGG 1460  
 Db 1201 ATGACAAAGTTGAAAAACAGCCCTGCAGAGACAGAGATTATGCTGCAACAGGTGAGTGG 1260  
 Qy 1461 GTGATATGATTAAGAGATCATTTGACCCCTGTCAAAAGTACAGATGAGGCTTCAA 1520  
 Db 1261 GTGATATGATTAAGAGATCATTTGACCCCTGTCAAAAGTACAGATGAGGCTTCAA 1320  
 Qy 1521 AATGACAGCTCTTGATGATGATTTATTTGACAAACAGAGAGTGTGCTATTAACCT 1580  
 Db 1321 AATGACAGCTCTTGATGATGATTTATTTGACAAACAGAGAGTGTGCTATTAACCT 1380  
 Qy 1581 GAACAGCTACGCCAGGCCCAATGCCAGACAGTATGATTCAGAAATGATGAGTGG 1639  
 Db 1381 GAACAGCTACGCCAGGCCCAATGCCAGACAGTATGATTCAGAAATGATGAGTGG 1439

RESULT 4  
 AAH56862  
 ID AAH56862 standard: DNA: 1306 BP.  
 AC AAH56862:  
 DT 06-SEP-2001 (first entry)  
 DE Antibiotic resistant S. pyogenes groEL gene partial sequence SEQ ID# 8.  
 XX  
 OS Streptococcus pyogenes.  
 XX  
 PN W0200136625-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 20-NOV-2000: 2000MO-CA01347.  
 XX  
 PR 18-NOV-1999: 990S-0166249.  
 XX

PA (GENE-) GENESENSE TECHNOLOGIES INC. 1  
 XX Wright JA, Young AH, Dugourd D:  
 PI WPI: 2001-355633/37.  
 XX  
 DR  
 XX  
 PT Novel antisense compounds targeting nucleic acid encoding groEL or  
 PT groES gene of microorganism, which hybridize with and inhibit  
 PT expression of the genes, useful to inhibit growth of microorganism  
 PT having the genes -  
 PS Disclosure: Fig 8; 110pp: English.  
 XX  
 CC The present invention specifically claims AAH56862 to AAH56832 which are  
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More  
 CC generally, antisense compounds (I) comprising antisense oligonucleotides  
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat  
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a  
 CC microorganism, where the antisense compound is complementary to GL or  
 CC GS of a microorganism and specifically hybridizes with and inhibits the  
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral  
 CC and antiproliferative activities, and can be used in antisense therapy  
 CC and for inhibition of expression of groE or groEL. (I) are useful for  
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are  
 CC also useful for inhibiting the growth of a microorganism, or inhibiting  
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or  
 CC a virus) having a GL or GS gene which involves administering to the  
 CC microorganism or to a cell infected with the microorganism (I) (I) are  
 CC also useful for treating a mammalian pathological condition mediated by  
 CC the microorganisms which involves identifying a eukaryotic organism  
 CC having a pathological condition mediated by microorganisms having a GL  
 CC or GS gene and administering (I) such that the growth of microorganism  
 CC is inhibited. The antisense compounds are utilized for diagnostics,  
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
 CC prevent or delay microbial infections in humans. They are also useful as  
 CC molecular weight markers. AAH56862 to AAH56832 and AAH56833 to AAH56854  
 CC represent PCR primers for groE sequences which are used in the  
 CC exemplification of the present invention. AAH56855 to AAH56870 represent  
 CC groE nucleotide sequence given in the present invention.  
 XX  
 SQ Sequence 1306 BP; 407 A; 235 C; 308 G; 356 T; 0 other;

Query Match 68.7%; Score 1140.4; DB 22; Length 1306;  
 Best Local Similarity 99.9%; Pred. No. 7.6e-289;  
 Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 498 GAAGCTATGAGCGGTGGGCAACGATGCTGATTAACATCCAGAAATCTCGAGATG 557  
 Db 2 GAAGCTATGAGCGGTGGGCAACGATGCTGATTAACATCCAGAAATCTCGAGATG 61  
 Qy 558 GAAACAGAACTGAAGTGGTGAAGCATGCAATTTGACCGTGTACTCTGCAATAC 617  
 Db 62 GAAACAGAACTGAAGTGGTGAAGCATGCAATTTGACCGTGTACTCTGCAATAC 121  
 Qy 618 ATGCTCAGACAGCAATGAAAAATGCTTGACAGCTTGAACCCATTTATCTTAACAG 677  
 Db 122 ATGCTCAGACAGCAATGAAAAATGCTTGACAGCTTGAACCCATTTATCTTAACAG 181  
 Qy 678 GATTAATAAGTGCATAACATCCAGACATTTTGCCACTACTGTAGAGAGTTCTTAAC 737  
 Db 182 GATTAATAAGTGCATAACATCCAGACATTTTGCCACTACTGTAGAGAGTTCTTAAC 241  
 Qy 738 AACGCTCATTAATCTATTATGAGATGATGATGATGATGATGATGATGATGATGAT 797  
 Db 242 AACGCTCATTAATCTATTATGAGATGATGATGATGATGATGATGATGATGATGAT 301  
 Qy 798 TTGAACAAGATTCGTGCTGATTTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTG 857  
 Db 302 TTGAACAAGATTCGTGCTGATTTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTG 361  
 Qy 858 CGTGTAAAGCTATGCTGATGAGACATTTGATGCTGACAGGTGATGATGATGATGATG 917  
 Db 362 CGTGTAAAGCTATGCTGATGAGACATTTGATGCTGACAGGTGATGATGATGATGATG 421

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OY 918 GATGTAGAGCTTGAATTAAGATGCTACANTGACAGCCCTTGAGAGCTGCTAAGATT 977
    |||||||
DB 422 GATGTAGAGCTTGAATTAAGATGCTACANTGACAGCCCTTGAGAGCTGCTAAGATT 481
OY 978 ACAGTTGATAAAGATGACAGATTAATTTGAGAGTTCAGAGATTCAGAGCTTATGCT 1037
    |||||||
DB 482 ACAGTTGATAAAGATGACAGATTAATTTGAGAGTTCAGAGATTCAGAGCTTATGCT 541
OY 1038 AACCGTATGCACTGATTAATTCGCAATTAAGAAACAACAACTTCTGACTTACCGTGAA 1097
    |||||||
DB 542 AACCGTATGCACTGATTAATTCGCAATTAAGAAACAACAACTTCTGACTTACCGTGAA 601
OY 1098 AAATCTCAAGAACCTTTGGCGAAATTAAGCTGTGTGTTAGCTTTATCAAGTAGAGACT 1157
    |||||||
DB 602 AAATCTCAAGAACCTTTGGCGAAATTAAGCTGTGTGTTAGCTTTATCAAGTAGAGACT 661
OY 1158 CCAACAGACAGAGCTTTAAAGAAATGAACCTTGCAATGAGATGCTTAAATGCTACA 1217
    |||||||
DB 662 CCAACAGACAGAGCTTTAAAGAAATGAACCTTGCAATGAGATGCTTAAATGCTACA 721
OY 1218 CGTGCAGAGCTTGAAGAGATTCCTGCTGCTGTGTGAGACAGCACTTATTCAGGTTATT 1277
    |||||||
DB 722 CGTGCAGAGCTTGAAGAGATTCCTGCTGCTGTGTGAGACAGCACTTATTCAGGTTATT 781
OY 1278 GAAAAAGTAGAGAGCTTGTGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1337
    |||||||
DB 782 GAAAAAGTAGAGAGCTTGTGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
OY 1338 CGTGCCTGAAGAGAGCTTGTGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1397
    |||||||
DB 842 CGTGCCTGAAGAGAGCTTGTGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901
OY 1398 GTTATGACAGATGTAAGAAAGCCCTGCGAGAGACAGATTAATCTGCAACAGGTGAG 1457
    |||||||
DB 902 GTTATGACAGATGTAAGAAAGCCCTGCGAGAGACAGATTAATCTGCAACAGGTGAG 961
OY 1458 TGGGTTGATGATTAAGACAGAAATCATGACCTGTCAAGAGTAACAGATGAGCGCTT 1517
    |||||||
DB 962 TGGGTTGATGATTAAGACAGAAATCATGACCTGTCAAGAGTAACAGATGAGCGCTT 1021
OY 1518 CAATATGACAGCTTGTAGCTAGTCTTATTTTGTACACAGAGACAGTGTGCTATATAA 1577
    |||||||
DB 1022 CAATATGACAGCTTGTAGCTAGTCTTATTTTGTACACAGAGACAGTGTGCTATATAA 1081
OY 1578 CCTGAACAGAGTACAGCCAGCCAGCAAGTCCAGAGAGTATGATCCAGAGATGATGGCT 1637
    |||||||
DB 1082 CCTGAACAGAGTACAGCCAGCCAGCAAGTCCAGAGAGTATGATCCAGAGATGATGGCT 1141
OY 1638 GG 1639
    ||
DB 1142 GG 1143

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## RESULT 5

AAH56865 standard; DNA; 1305 BP.

ID AAH56865;

06-SEP-2001 (first entry)

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DE Antibiotic resistant S. pyogenes groEL gene partial sequence SEQ ID:11.
XX
XX Antisense oligonucleotide; groEL; groEL; groEL; inhibitor; growth;
XX microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
XX Streptococcus pyogenes; Staphylococcus aureus; pseudomonas aeruginosa;
XX antibacterial; antiviral; antiproliferative; antisense therapy;
XX microbial infection; ds.
OS Streptococcus pyogenes.
XX
XX WO200136635-A2.
PN

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XX 25-MAY-2001.
XX
XX 20-NOV-2000; 2000MO-CA01347.
XX
XX 18-NOV-1999; 9905-0166249.
XX
XX (GENE-) GENSENSE TECHNOLOGIES INC.
XX
XX Wright JA, Young AH, Dugourd D;
XX WPI: 2001-355633/37.
XX
XX Novel antisense compounds targeting nucleic acid encoding groEL or
XX groEL gene of microorganism, which hybridize with and inhibit
XX expression of the genes, useful to inhibit growth of microorganism
XX having the genes -
XX
XX Disclosure: Fig 11; 110pp; English.
XX
XX The present invention specifically claims AAH56368 to AAH56832 which are
XX antisense oligonucleotides to nucleotide sequences encoding groEL. More
XX generally, antisense compounds (I) comprising antisense oligonucleotides
XX of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
XX shock protein (HSP160) (G1) and groES (HSP10) (G5) gene from a
XX microorganism, where the antisense compound is complementary to G1 or
XX G5 of a microorganism and specifically hybridizes with and inhibits the
XX expression of G1 or G5, is claimed. (I) have antibacterial, antiviral
XX and antiproliferative activities, and can be used in antisense therapy
XX and for inhibition of expression of groES or groEL. (I) are useful for
XX inhibiting expression of G1 or G5 in cells or tissues in vitro. (I) are
XX also useful for inhibiting the growth of a microorganism, or inhibiting
XX the expression of G1 or G5 gene in a microorganism (a bacterial cell or
XX a virus) having a G1 or G5 gene which involves administering to the
XX microorganism or to a cell infected with the microorganism, (I). (I) are
XX also useful for treating a mammalian pathological condition mediated by
XX the microorganisms which involves identifying a eukaryotic organism
XX having a pathological condition mediated by microorganisms having a G1
XX or G5 gene and administering (I) such that the growth of microorganism
XX is inhibited. The antisense compounds are utilized for diagnostics,
XX therapeutics, prophylaxis and as research reagents and kits, e.g., to
XX prevent or delay microbial infections in humans. They are also useful as
XX molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
XX represent PCR primers for groEL sequences which are used in the
XX exemplification of the present invention. AAH56855 to AAH56870 represent
XX groEL nucleotide sequence given in the present invention.
XX
XX Sequence 1305 BP: 406 A; 238 C; 312 G; 349 T; 0 other:
XX
XX Query Match 67.6%; Score 1122.6; DB 22; Length 1305;
XX Best Local Similarity 99.2%; Pred. No. 3.6e-284;
XX Matches 1128; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 503 TATGAGCGCTGTGGCAAGATGTGTGATTACATCGAAGAACTCGAGGTGGAAC 562
    |||||||
DB 1 TATGAGCGCTGTGGCAAGATGTGTGATTACATCGAAGAACTCGAGGTGGAAC 60
OY 563 AGAAGCTTGAAGTGTGAGGATGCAATTTGACCGTGTGCTGCTCATATATGCT 622
    |||||||
DB 61 AGAAGCTTGAAGTGTGAGGATGCAATTTGACCGTGTGCTGCTCATATATGCT 120
OY 623 CACAGCATGTAAGAAATGTTGCGAGACCTTGAAGAAACCATTTATCTTAATACGGATA 662
    |||||||
DB 121 CACAGCATGTAAGAAATGTTGCGAGACCTTGAAGAAACCATTTATCTTAATACGGATA 180
OY 663 AAAAGTGTCAACATCCAGACATTTTGCACACTGTTAGAGAGCTTTAAACCAACGG 742
    |||||||
DB 181 AAAAGTGTCAACATCCAGACATTTTGCACACTGTTAGAGAGCTTTAAACCAACGG 240
OY 743 TCATTAATCATTAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 802
    |||||||
DB 241 TCATTAATCATTAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

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Best Local Similarity 79.2%, Pred. No. 2.4e-268;  
Matches 1274; Conservative 0; Mismatches 331; Indels 3; Gaps 1;

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Oy 15 ATGGCAAAAGAAATCAATTTTCACAGATGCGCGTGTCCATGTGGCGGAGTTGAT 74
Db 1 ATGGCAAAAGATTTAAATTTTCACAGATGCGCGTGTCCATGTGGCGGAGTTGAT 60
Oy 75 ATTTTACGATACGCTCAAGTAAAGCTGTCTTAAAGGGCGCAATGTGTTGAA 134
Db 61 ATTTTACGATACGCTCAAGTAAAGCTGTCTTAAAGGGCGCGTAAATGTGTTGAA 120
Oy 135 AAACTTTGGTTCCTCTTAATTAATGACGGGTAAACATGTCTTAAAGATCGAA 194
Db 121 AAAGCATTTGGTTCCTCTTAATTAATGACGGGTAAACATGTCTTAAAGATCGAA 180
Oy 195 TTGAAGATCATTTTGAACATGAGAGCAAAATGTGTCTGTAAGTGGCTCTTAAAC 254
Db 181 CTGAAGATCATTTTGAACATGAGAGCTTAACTGTGTCTGTAAGTGGCTCTTAAAC 240
Oy 255 AATGATTTGGTGTGATGGAGACATGCAAGATTTGACAAACCATTTGTCAT 314
Db 241 AATGATTTGGAGGATGGAGACATGCAAGCTGCTTTTGAACCAAGCTTATGTGCG 300
Oy 315 GAAGCACTAAAAATGTGACAGCAGTGTCAATCCAAATGTGTATCCGTGAGGCAATTGAA 374
Db 301 GAAGCTCTTAAAAATGTGACAGCAGTGTCAATCCAAATGTGTATCCGTGATTTGAA 360
Oy 375 ACAGCAACAGCAACAGCTGTGAAAGCCTTGAAGCCATTTGCTAACCTGTATGCGCAAG 434
Db 361 ACAGCTGTTTACAGCAGCAGTGTGAAAGCCTTGAAGCCATTTGCTAACCTGTATGCGCAAA 420
Oy 435 GAAGCTATTGCTGAGGTGCTGCAATATCATCAGCTGTGAAAGATTTGAGAGATTAATAC 494
Db 421 GAAGCTATTGCTGAGGTGCTGCAATATCATCAGCTGTGAAAGATTTGAGAGATTAATAC 480
Oy 495 TCAGAACTATGAGAGGCTGTGGCAAGATGTGTGATACATGCAAGATTCAGAGGT 554
Db 481 TCTGAAGCTATGAGAGGCTGTGGCAAGATGTGTGATACATGCAAGATTCAGAGGT 540
Oy 555 ATGSAACAGAACTGTAAGTGTGAAAGCATTTGACCGTGTACCTGTCTCAA 614
Db 541 ATGSAACAGAACTGTAAGTGTGAAAGCATTTGACCGTGTACCTGTCTCAA 600
Oy 615 TACATGCTACAGACATGAAAAATGGTTGCAGACCTGAAACCCATTTATCTTAATC 674
Db 601 TATATGCTACATGATACGAGAAAAATGGTTGCAGACCTGAAACCCATTTATCTTAATC 660
Oy 675 ACGGATAAAAAGTGTCAAAACATCCAAAGACATTTTGGCCTACTTGTAGAGAGTTCTTAA 734
Db 661 ACGGATAAAAAGTGTCAAAACATCCAAAGATTTTGGCCTACTTGTAGAGAGTTCTTAA 720
Oy 735 ACCAAGCTGCATTAATCATTAATGAGATGATGATGATGATGATGATGATGATGATGAT 794
Db 721 ACAAATGCTGCATTAATCATTAATGAGATGATGATGATGATGATGATGATGATGATGAT 780
Oy 795 GTCTTGAACAAAGTGTGCTGATCTTCAATGCTGTGCTCAAGGCGCGAGATTTGCT 854
Db 781 GTTCTTGAACAAATGCTGGAACCTTCAATGCTGTGCTTAAAGCCCTGGAATTTGCT 840
Oy 855 GATGCTGTAAAGCTATGCTGAAAGCATTTGCTGTAAGTGTGAGAGGCTGATGATGATGAT 914
Db 841 GATGCTGTAAAGCATGCTGAAAGCATTTGCTGTAAGTGTGAGAGGCTGATGATGATGATGAT 900
Oy 915 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 974
Db 901 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Oy 975 ATTACAGTGTATTAAGATGACAGCAATGTTGTTGAGAGTTCAGAGTTCAGAGTAT 1034
Db 961 GTACAGTGTATTAAGATGACAGCAATGTTGTTGAGAGTTCAGAGTTCAGAGTAT 1020
Oy 1035 GCTAACCGTATTTGACATGATTAATGCAATTAAGAAACAACTTGTGACTTGAACCT 1094
Db 1021 GCTAACCGTATTTGACATGATTAATGCAATTAAGAAACAACTTGTGACTTGAACCT 1080
Oy 1095 GAAAACTACAGAAAGCTTTGGCGAAATTAAGTGTGTGATGATGATGATGATGATGATGATGAT 1154
Db 1081 GAAAAATTTACAGAAAGCTTTGGCGAAATTAAGTGTGTGATGATGATGATGATGATGATGATGAT 1140
Oy 1155 GCTCAGACAGACAGCTTTTAAAGAAATGCAATGCTGATGATGATGATGATGATGATGATGATGAT 1214
Db 1141 GCAGCAGCTGAAACAGAAATTAAGAGATGAAATGCTGATGATGATGATGATGATGATGATGATGAT 1200
Oy 1215 ACAGTGTGAGCGGTGAAAGAGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1274
Db 1201 ACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Oy 1275 ATGAAAAAGTACAGCTCTTGAAGCTTGAAGCGCATGATGATGATGATGATGATGATGATGATGAT 1334
Db 1261 ATGAAAAAGTACAGCTCTTGAAGCTTGAAGCGCATGATGATGATGATGATGATGATGATGATGATGAT 1320
Oy 1335 CTTCGTGCTGTGAAGAGCTGTGACGCAAAATTTGCTTTAAATGCTGTGTGTGTGTGTGTGTGTGTGT 1394
Db 1321 CTTCGTGCTGTGAAGAGCTGTGACGCAAAATTTGCTTTAAATGCTGTGTGTGTGTGTGTGTGTGTGT 1380
Oy 1395 GTAGTATTTGACAGTTGAAAAACAGCCCTGACAGAAACAGATTTAAATGCTGTGTGTGTGTGTGT 1454
Db 1381 GTTATTTATGACGTTTAAACAGCTGCAAAATTTGATGATGATGATGATGATGATGATGATGATGAT 1440
Oy 1455 GAGTGGGTGATGATGATTTAAAGAGGATCATTTGACCTGTGCAAAAGTAAACAGATGACAGCG 1514
Db 1441 GAATGGGTGATGATGATTTAAAGAGGATCATTTGACCTGTGCAAAAGTAAACAGATGACAGCTTGTCA 1500
Oy 1515 CTTCAAAATGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1574
Db 1501 CTTCAAAATGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
Oy 1575 AAACCTGAAC---AGCTACGCGACGCGCAAGCAATGCGAGAGATGATGATGATGATGATGATGATGAT 1619
Db 1561 AAACCTGAACGAGAGCTCTACAGCTGTGCAATGATGATGATGATGATGATGATGATGATGATGAT 1608

RESULT 8
AAH86153
ID AAH86153 standard; DNA; 1654 BP.
XX
AC AAH86153;
XX
DT 22-SEP-1999 (first entry)
XX
DE DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-2.
XX
KW Heat shock protein; Hsp60-2; Immune response; Immunological carrier;
XX
KW cancer control; tumour; sarcoma; cancer; gene therapy; sf.
XX
OS Streptococcus pneumoniae.
XX
PN MO9935270-A1.
XX
PD 15-JUL-1999.
XX
PF 29-DEC-1998; 98MO-CA01203.
XX
PR 31-DEC-1997; 97US-0001737.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Mizzen L, Walsniewski J;
XX
DR WPI: 1999-430397/36.
XX
DR P-PSDB: AAY23902.
XX
PT New nucleic acid encoding heat shock protein-60 from Streptococcus,
XX
PT useful in vaccines, as carriers for other immunogens, as anticancer
XX
PT agents and for diagnosis

```

PS Claim 3; Fig 2a-b; 176bp; English.

XX The present sequence encodes a heat shock protein, designated Hsp60-2.

CC The protein, its fragments, variants and fusion proteins, are

CC used to elicit or enhance an immune response against Streptococcus,

CC and to elicit a similar response to a target antigen fused to the

CC protein. Unlike other immunological carriers, Hsp60 proteins are not

CC immunosuppressive so provide an increased response to any conjugated or

CC effects associated with endotoxins. They can also be used to detect

CC specific antibodies and in treatment or prevention of tumours

CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or

CC liver). The Hsp60 polynucleotide is used for recombinant production

CC of the protein, as a source of primers and probes for detecting

CC streptococci in standard hybridization/amplification assays, and

CC therapeutically in gene therapy vectors.

XX

SO Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;

Query Match 53.3%; Score 1052; DB 20; Length 1654;

Best Local Similarity 77.7%; Fred. No. 1.3e-265;

Matches 1271; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

DB 1 GAATTCGGCTTCATATGTCGCAAAAGAAATCAATTTTACAGCATGCGCGTCCCATGG 60

DB 1 GAATTCGGCTTCATATGTCGCAAAAGAAATCAATTTTACAGCATGCGCGTCCCATGG 60

QY 61 TCGCGGAGTTGATATGTAGCAGATACCGTCAAGTGTGCTCAAGGCGCA 120

DB 61 TCGCGGAGTTGATATGTAGCAGATACCGTCAAGTGTGCTCAAGGCGCA 120

QY 121 ATGTTGTTCTGAAAAAGCTTTGGTCTCCCTTAATTAATGAGGCGGATACATG 180

DB 121 ATGTTGTTCTGAAAAAGCTTTGGTCTCCCTTAATTAATGAGGCGGATACATG 180

DB 121 ATGTTGTTCTGAAAAAGCTTTGGTCTCCCTTAATTAATGAGGCGGATACATG 180

QY 181 CTAAAGATGCAATTAAGAGATCAATTTGAAAGATGGGCAAAATTTGGTCTGAG 240

DB 181 CTAAAGATGCAATTAAGAGATCAATTTGAAAGATGGGCAAAATTTGGTCTGAG 240

DB 181 CTAAAGATGCAATTAAGAGATCAATTTGAAAGATGGGCAAAATTTGGTCTGAG 240

QY 241 TGGCTCTTAAACCAATGATTTGCTGTATGCGACACTACGCAAGTTTGAC 300

DB 241 TGGCTCTTAAACCAATGATTTGCTGTATGCGACACTACGCAAGTTTGAC 300

DB 241 TGGCTCTTAAACCAATGATTTGCTGTATGCGACACTACGCAAGTTTGAC 300

QY 301 AAGCATTCTTCATGAGAGCACTAAATGTAAGAGGCTGTAATGCAATTTGATCC 360

DB 301 AAGCATTCTTCATGAGAGCACTAAATGTAAGAGGCTGTAATGCAATTTGATCC 360

DB 301 AAGCATTCTTCATGAGAGCACTAAATGTAAGAGGCTGTAATGCAATTTGATCC 360

QY 361 ATGCAATCTGCTGGAAGGAAATCAAAAGCTGACAGAGGTCMAATTCGATATTC 360

DB 361 ATGCAATCTGCTGGAAGGAAATCAAAAGCTGACAGAGGTCMAATTCGATATTC 360

DB 361 ATGCAATCTGCTGGAAGGAAATCAAAAGCTGACAGAGGTCMAATTCGATATTC 360

QY 421 CTGATCTGCAAGAGATGCTATGCTGAGCGCTGAGTATCATCAGCTGTGAAAAG 480

DB 421 CTGATCTGCAAGAGATGCTATGCTGAGCGCTGAGTATCATCAGCTGTGAAAAG 480

DB 421 CTGATCTGCAAGAGATGCTATGCTGAGCGCTGAGTATCATCAGCTGTGAAAAG 480

QY 481 TTGAGAGATATCTGAGAGATGAGAGGCTGTGGGCAAGATGCTGATATTCATG 540

DB 481 TTGAGAGATATCTGAGAGATGAGAGGCTGTGGGCAAGATGCTGATATTCATG 540

DB 481 TTGAGAGATATCTGAGAGATGAGAGGCTGTGGGCAAGATGCTGATATTCATG 540

QY 541 AAGATCTGAGGATGAGAGAGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTG 600

DB 541 AAGATCTGAGGATGAGAGAGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTG 600

DB 541 AAGATCTGAGGATGAGAGAGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTG 600

QY 601 GTTACCTGCTCATATCATGCTGACAGCAATGAAAAATGTTGACAGCTTGAAC 660

DB 601 GTTACCTGCTCATATCATGCTGACAGCAATGAAAAATGTTGACAGCTTGAAC 660

DB 601 GTTACCTGCTCATATCATGCTGACAGCAATGAAAAATGTTGACAGCTTGAAC 660

QY 661 CATTTATCTTAATCAGAGATAAAAAGTGCACAATCCAGAGATTTGGCAGACTT 720

DB 661 CATTTATCTTAATCAGAGATAAAAAGTGCACAATCCAGAGATTTGGCAGACTT 720

DB 661 CATTTATCTTAATCAGAGATAAAAAGTGCACAATCCAGAGATTTGGCAGACTT 720

QY 721 AGAAGTCTTAAGCAACGCTCATCTACTATTTGAGATGATGATGATGATG 780

DB 721 AGAAGTCTTAAGCAACGCTCATCTACTATTTGAGATGATGATGATGATGATG 780

DB 721 AGAAGTCTTAAGCAACGCTCATCTACTATTTGAGATGATGATGATGATGATG 780

DB 721 AAGAGTCTTAAGCAACGCTCATCTACTATTTGAGATGATGATGATGATG 780

QY 781 CACTTCCAACTGCTGTTGAAACAGATTCGTGACTTTCATATGCTGCTTAAAG 840

DB 781 CACTTCCAACTGCTGTTGAAACAGATTCGTGACTTTCATATGCTGCTTAAAG 840

DB 781 CACTTCCAACTGCTGTTGAAACAGATTCGTGACTTTCATATGCTGCTTAAAG 840

QY 841 CCCAGAGTTTGGTGTATGCTGAAAGATGCTGAAAGATGCTGCTTAAAG 900

DB 841 CCCAGAGTTTGGTGTATGCTGAAAGATGCTGAAAGATGCTGCTTAAAG 900

DB 841 CCCAGAGTTTGGTGTATGCTGAAAGATGCTGAAAGATGCTGCTTAAAG 900

QY 901 GTACAGATATACAGAGATATGAGCTGATTAAGATGCTGCTTAAAG 960

DB 901 GTACAGATATACAGAGATATGAGCTGATTAAGATGCTGCTTAAAG 960

DB 901 GTACAGATATACAGAGATATGAGCTGATTAAGATGCTGCTTAAAG 960

QY 961 GACAGGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1020

DB 961 GACAGGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1020

DB 961 GACAGGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1020

QY 1021 GTTGAAGATATGCTATACAGATTAAGATTAAGATTAAGATTAAGATTAAG 1080

DB 1021 GTTGAAGATATGCTATACAGATTAAGATTAAGATTAAGATTAAGATTAAG 1080

DB 1021 GTTGAAGATATGCTATACAGATTAAGATTAAGATTAAGATTAAGATTAAG 1080

QY 1081 CTGACTTTGACGCTGAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1140

DB 1081 CTGACTTTGACGCTGAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1140

DB 1081 CTGACTTTGACGCTGAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1140

QY 1141 TTATCAAGATGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200

DB 1141 TTATCAAGATGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200

DB 1141 TTATCAAGATGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200

QY 1201 ATGCTCTTAATGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

DB 1201 ATGCTCTTAATGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

DB 1201 ATGCTCTTAATGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

QY 1261 CACTTATTAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320

DB 1261 CACTTATTAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320

DB 1261 CACTTATTAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320

QY 1321 GACCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

DB 1321 GACCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

DB 1321 GACCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

QY 1381 GGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

DB 1381 GGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

DB 1381 GGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

QY 1441 ATGCTGCAAG 1500

DB 1441 ATGCTGCAAG 1500

DB 1441 ATGCTGCAAG 1500

QY 1501 TGAAGCTTGAAG 1560

DB 1501 TGAAGCTTGAAG 1560

DB 1501 TGAAGCTTGAAG 1560

QY 1561 CAGTGTGTAATTAAG 1620

DB 1561 CAGTGTGTAATTAAG 1620

DB 1561 CAGTGTGTAATTAAG 1620

QY 1621 ATCCAGAGATGATGAG 1636

DB 1621 ATCCAGAGATGATGAG 1636

DB 1621 ATCCAGAGATGATGAG 1636

RESULT 9

AAH90800

ID AAH90800 standard; DNA; 1623 BP.

XX

AC AAH90800;

XX

DE 02-Oct-2001 (first entry)

XX

DE CFE 104 coding sequence.

XX

KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability;  
 KW CPE; CEG; Conserved Essential Gene; bacterial infection;  
 KW antisense therapy; antibiotic resistance; ds.  
 OS Streptococcus pneumoniae.  
 PN W0200149721-A2.  
 XX 12-JUL-2001.  
 PD 29-DEC-2000; 2000MO-US35604.  
 PF 30-DEC-1999; 99US-0174089.  
 PR (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucoleri RE;  
 PI Thanasil JA;  
 DR MPI; 2001-496721/54.  
 XX P-PSDB; AAM01101.  
 PT Nucleic acids encoding conserved essential genes involved in bacterial  
 PT replication which are potential targets for the treatment of antibiotic  
 PT resistant bacterial infections -  
 XX  
 PS Claim 16; Page 231; 380pp; English.  
 XX  
 CC The present invention relates to nucleic acids (AAH90701-AAH90918)  
 CC encoding polypeptides (AAM01002-AAM01114), which are essential for the  
 CC viability of a bacterial cell wall. The acronym CEG stands for "CEG For  
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic  
 CC acids are useful for detecting the presence of proteins essential for the  
 CC viability of a bacterial cell wall in samples such as cells, tissues,  
 CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,  
 CC and for detecting corresponding target nucleic acid molecules with  
 CC complementary sequences. The nucleic acids are also useful for  
 CC determining whether a genomic nucleotide sequence of interest is  
 CC essential for viability of a bacterial cell or whether it resides within  
 CC an operon, by integrating an exogenous nucleotide sequence comprising a  
 CC portion of an open reading frame of the genomic sequence of interest  
 CC (comprising 200-500 base pairs) into the genomic sequence of interest  
 CC which confers a selectable phenotype to the cell, and determining cell  
 CC viability with a selection agent such as chloramphenicol. The nucleic  
 CC acids and proteins are also useful as vaccines and for treating bacterial  
 CC infections with gene therapy and antisense therapy. The nucleic acids  
 CC also enable identification of targets suitable for the treatment of  
 CC antibiotic resistant bacterial infections.  
 CC  
 SO Sequence 1623 BP; 490 A; 325 C; 394 G; 414 T; 0 other;  
 Query Match 62.6%; Score 1039.2; DB 22; Length 1623;  
 Best Local Similarity 77.6%; Pred. No. 2,9e-262;  
 Matches 1257; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

Db 241 AATGATATTCGAGGTGAGGAGCACTACGACTGCAACAGCTTTGACCCCAAGCATTCGTCCT 300  
 Qy 315 GAAGAGCTAAAAATGTGACACGACGCTGCTAATCAATGGTATCGTCGAGCGATTGAA 374  
 Db 301 GAAGGATCAAAAACGTCACAGCAGGTGCAAAATCCAAATGGTATGCTGCGATTGAA 360  
 Qy 375 ACAGCAACGACGACGCTGTGAACCTTGAAAGCCATTCGATATCGTGGCAAG 434  
 Db 361 ACAGCAGTTGCCGACGAGCTTGAACCTTGAAAGCCATTCGATATCGTGGCAAG 420  
 Qy 435 GAAGCTATTTGCTGACGCTGCTGAGTATCAATCAATCGTGAAGAAATGGGAGATATATC 494  
 Db 421 GAAGCTATTTGCTGACGCTGCTGAGTATCAATCAATCGTGAAGAAATGGGAGATATC 480  
 Qy 495 TCAGAACTATGAGCGCTGTGGGCAAGCATGCTGTGATTCATCAATCAAGATCTCGAGGT 554  
 Db 481 TCTGAAAGCAATGGAAGAAAGTGGCAAGACGCTGATCACCATCGAAGATCAAGTGGT 540  
 Qy 555 ATGGAACAGAACTGGAAGTGGTGAAGGCAATTCGACGCTGTTACCTGCTCA 614  
 Db 541 ATGGAACAGAACTGGAAGTGGTGAAGGCAATTCGACGCTGTTACCTGCTCA 600  
 Qy 615 TACATGCTCAGCAGCAATGAAAAATGTTGACAGACTTGAAAAACCATTTATCTTATTC 674  
 Db 601 TACATGCTGACAGATGAGCAAAAAATGTTGCTGACCTTGAAAAATCCTGACATTTGAT 660  
 Qy 675 ACGATAAAAAAGTGCACAACTCCAGACATTTTGGCAGTCTGAGGAAGTCTTAA 734  
 Db 661 ACGACAGAAAAATTTCCAAATCCAGAAATTTGACATTTTGGAAAGATTTCTCA 720  
 Qy 735 ACCAAGCTGCTATCTCATTTATTCAGATGAGTGGTGAAGCACTTCAACCTT 794  
 Db 721 AGCAATCTCCACCTCTGATTTTTCGAGATGATGATGATGATGATGATGATGATGAT 780  
 Qy 795 GTCCTGACAAAGTTCGTGTGATTTAATGATGATGATGATGATGATGATGATGATGAT 854  
 Db 781 GTTTTGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 Qy 855 GATCGCTAAACCTATGCTTGAAGACATTCGATTTGACAGGTGATGATGATGATGAT 914  
 Db 841 GACCTGCTAAACCTATGCTTGAAGACATTCGATTTGACAGGTGATGATGATGATGAT 900  
 Qy 915 GAGGATCTAGACCTGATTAATTAAGATGCTAATGACAGCCTTGACAGGTGATGAT 974  
 Db 901 GAGGATCTAGACCTGATTAATTAAGATGCTAATGACAGCCTTGACAGGTGATGAT 960  
 Qy 975 ATTACAGTATTAAGATGACAGATTAATGATGATGATGATGATGATGATGATGATGAT 1034  
 Db 961 GTGACCTGACAAAGATAGCAAGTATTAATGATGATGATGATGATGATGATGATGAT 1020  
 Qy 1035 GCTAACGCTATTCATGATTAATGCAATTAAGCAACCACTTGCATTTGACAGCT 1094  
 Db 1021 TCTGACGCTGCTGCTGATTAATGCAATTAAGCAACCACTTGCATTTGACAGCT 1080  
 Qy 1095 GAAACACTACAAAGATTTGGCAATTAAGTGTGCTGATGCTGATGATGATGATGAT 1154  
 Db 1081 GAAACACTACAAAGATTTGGCAATTAAGTGTGCTGATGCTGATGATGATGATGATGAT 1140  
 Qy 1155 GCTCCACAGACAGCTTTAAAGAAATGAATTCGATTTGATGATGATGATGATGAT 1214  
 Db 1141 GCGGCACTAAACCTGATTAAGAAATGAATTCGATTTGATGATGATGATGATGAT 1200  
 Qy 1215 ACACGTGACCCCTTGAAGAGTATGCTGCTGATGATGATGATGATGATGATGATGAT 1274  
 Db 1201 ACTGCTGACCTTGAAGAGTATGCTGCTGATGATGATGATGATGATGATGATGAT 1260  
 Qy 1275 ATGGAAGAAATGACAGCTTGAAGAGTATGCTGCTGATGATGATGATGATGATGAT 1334  
 Db 1261 ATTCACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
 Qy 1335 CTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1394  
 Db 1321 CTCGCTGCTTGAAGAACCGCTTGCATTAATGCTGATGATGATGATGATGATGATGAT 1380

QX	Sequence	1926 BP: 585 A; 382 C; 464 G; 495 T; 0 other:
SQL	Query Match	62.5%; Score 1038.4; DB 22; Length 1926;
	Best Local Similarity	77.5%; Pred. No. 56-262;
	Matches 1258; Conservative	0; Mismatches 366; Indels 0; Gaps 0;
QY	15	ATGGCAAAAGAAATCAAAATTTTCAGACATACCGGCGTCGCGCATAGGCGCGGAGTGTAT 74
DB	1	ATGGCAAAAGAAATTTAAATTTTATATCAATATCCCGTTCAGCTATATGCTCGTGATGCAT 60
QY	75	ATGTTACGAGATACCGTCAAAAGTAAACCGTGGTCTTAAAGGGCCGCAATGTTGTTGAA 134
DB	61	ATCTTCACGATACGATGTTAAAGTAACTTTGGGACAAAAGGTCGCATATGCTTTGAA 120
QY	135	AAAGCTTTGGTCTCCCTTAATTTACTATAGCGGGGTAAACCATTTGCTAAAGATCGAA 194
DB	121	AAGCATATGGGTTACCCCTTGATTAACCAATACGCGGTGACATATTGGCAAGAAATTA 180
QY	195	TTAGAAATCATTTTGAAGAAACATGGAGACCAAAATTTGGTCTGAAAGGCGCTCTTAAAC 254
DB	181	TTAAGAAACCATTTTGAAGAAATTAATGGGTGCGCAAAATGGTATCGAAGATAGCTTCA 240
QY	255	AATGATATTGCTGGTGTATGGGAGACGACTCTGCAACAGTTTGGACACAGCAATTTTCAT 314
DB	241	AATGATATGCGAGTGTATGGGAGACTCAACTGCAACTGTTTGGACCCAGCAATCTCGGT 300
QY	315	GAAAGACATTAATAAATGTGACAGAGAGTCTATATCAATATGGATATCGTGAGGACTTAA 374
DB	301	GAAAGATCAAAAACGTCACAGGAGTGCAAATTCGAATCGATATCGTGTGGATTA 360
QY	375	ACACAAACGCAACGCTGTTGAAGCTTGAAGCCATTGAACCATGTCACACCTGATCTGGCA 434
DB	361	ACACAGATTCGCCGACGACGATTAAGCTTGAAGAAACAGCTCCTGTTGTCATTA 420
QY	435	GAGCATTTTGCCTCAGGTGCGTGCATATCATCACTGCTGTAAGAAAGTTGGAGATATTC 494
DB	421	GAGCATTTTGCCTCAGGTGAGCGCGATATCTTCTGCTTGTGAAAGTTGGTAGATCATC 480
QY	495	TCAGAGCTATGAGACGCTGTGGGACGACGATGGTGTATTAACATCGAAGAAATCTGAGGT 554
DB	481	TCGGAAGCATGTGAAAAAGTTGGCAAAACGCGGTATCATCCATCGAAGATGACGTGT 540
QY	555	ATGGAACACGAATCTGAAGTGGTGAAGGCATCAATTTTGAACCGTGGTTACTGTCTCAA 614
DB	541	ATGGAACACGACCTTGAAGTGCATGAAGAGATCAAGTTTGAACCGTGGTTACTGTCTCAA 600
QY	615	TACATGGTACACGACATCGAAATTAATGGTTGACAGCTTGAAGAAACCATTTATCTTATC 674
DB	601	TACATGGTACACGATACGCAAAATTAATGGTGTGACCTTGAAGAAATCCGTAATTTTGAT 660
QY	675	ACGGATTAATAAAGTGTCAAAACATCCAAACATTTTCCACATCTTGAAGAGATCTTTAA 734
DB	661	ACGACACGATTAATCTATTTATTTGACAGATGATGGTGAAGAGACATCTCAACCTT 720
QY	735	ACCAACCGTCACTTACATTTATTTGACAGATGATGGTGAAGAGACATCTCAACCTT 794
DB	721	AGCAATCTCCACCTCTTGATATTTGCGATGATGATGGTGAAGAGACATCTCAACCTT 780
QY	795	GTCGTAAACAGATTCGTGTACTTCAATATGTGTGCTGTCAACAGCGCAGAGATTTGCT 854
DB	781	GTTTAAACAGATTCGTGTACTTCAACAGATGATGATGATGATGATGATGATGATGATGAT 840
QY	855	GATGCTGTAAAGCTATGCTTAAGACATTTGCTATTTTACAGAGTGTACAGTATTAACA 914
DB	841	GACGCTGTAAAGCTATGCTTAAGATATGCGCATTTTAACAGCGGACATTTATTAACA 900
QY	915	GAGATCTAGCACTGAAATTAATAAGATCTCAATGACAGCCCTTGGACAGGCTCTTAAG 974
DB	901	GAGACACTTGTGCTTGTAGTGAAGATGACAGCAATTTGAAGCTTGTGCTCAACAGCAGA 960
QY	975	ATTACAGTTGATTAAGATGACACAGATTAATTTGTTGAAGGTTAGGAGATTCAGAGCAT 1034

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Db	961	GTGACCGTGGACAAGATATGACAGCGGTTATTGTGAAAGGTGTAGAAATTCCTGAAGGATT	1020
Oy	1035	GCATCAACGGTATATGACATGATTAATATCCGATTTGAAATACAACTCTGACATTGGACCT	1094
Db	1021	TCATACCGGTGTGGGTTATCAAGTCCTCAATACGAACTACACACTTCTGTAATTTGACCGT	1080
Oy	1095	GAAATCAATCAAGAACGTTTGGCCGAATTTACGTGGTGTGTACTGTTTATCAAGTAGCA	1154
Db	1081	GAATATTTCCAGAACCCCTTGCCCAATTTGTCAAGTGGTGTGTACCGGTTATTTAAAGTCGGA	1140
Oy	1155	GCCTCAACAGAGACAGCTTTAAAGAAATGAACCTTGCAATTGAGATGCTCTAAATGCT	1214
Db	1141	CGCCCACTGAACTATGATTGAAAGAAATGAAATCACTCCCATTTGAAATGACCCCTCAACGCT	1200
Oy	1215	ACACGTGCAGCCGTTGAAGAGATATCGTTGCTGGTGGTGGAAACAGCACTATTACGGTT	1274
Db	1201	ACTGTGCAGCTGTTTGAAGAGATATGTGTGCAGGTGGTGGAAACAGCTCTTCCCAATGTG	1260
Oy	1275	ATTGAAAAAGTAGCAGCTTTGACTGTGAAGGCGATGATCTCATCGAGCATGATATTG	1334
Db	1261	ATTCCAGCTGTGGCTACCTTGGAAATTGACAGGATGATGACACAGAGCATATATTGT	1320
Oy	1335	CTTCGCGTCTAGAAAGACCTGTATGCTCAAAATTTGCTTTAAATGCTGGGTGAGAAAGCTCC	1394
Db	1321	CTCCGCGTGTGGAAACACTGTTCTGTCAAAATTTGCTCAACATGAGATTTGAAGGATCT	1380
Oy	1395	GTTGTTATTTAGCAAGTTGAAAAAACAAGCCCTGCAGAAACAGATTTAATGCTGCACAGCT	1454
Db	1381	ATGCTATTGCATCGTTTGAAGAAATGCTGAGACCTGGTATAGAGATTCAAGCGACAGACTGC	1440
Oy	1455	GAGTGGTGTGATATGATTTAAACAGAAATCATTTGACCTGTCAAAAGTAACAGCATGACG	1514
Db	1441	GAGTGGTATACATGATTGATCAAGAGATATTCATTCACAGTTAAAGTGAAGTGTAGCC	1500
Oy	1515	CTTCAAAATGACACTCTGTAGCTAGTCTTATTTTGACAACAGAAAGCAGTTGTTGCTAAT	1574
Db	1501	CTCAAAATGACACTCTGTAGCTAGTCTTATTTTGACAACAGAAAGCAGTGTAGGCCAAT	1560
Oy	1575	AAACTGAACTACAGCTACGCCAGCGCCAGCAATGCGACAGCAGATGATGATCCAGGAATGATG	1634
Db	1561	AAACCAAGAACACTAGACCCCAAGCTCCAGCAAGATGATCAAGATATATGAGGTGGAATGGCG	1620
Oy	1635	GGTG 1638	
Db	1621	GGAG 1624	
RESULT 11			
AAH56860			
ID	AAH56860	standard; DNA; 2107 BP.	
XX	AC		
XX	AAH56860;		
XX	06-SEP-2001	(first entry)	
DE	Antibiotic resistant S. pneumoniae groE operon sequence SEQ ID NO:6.		
KW	Antisense oligonucleotide; groE; groEL; groES; Inhibitor; growth;		
KW	Microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;		
KW	Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;		
KW	Antibacterial; antiviral; antiproliferative; Antisense therapy;		
KW	Microbial infection; ds.		
XX	Streptococcus pneumoniae.		
OS			
XX	MO200116625-A2.		
XX	25-MAY-2001.		
PD			
XX	20-NOV-2000; 2000MO-CA01347.		
XX			
XX	18-NOV-1999; 99US-0166249.		
XX			

(GENE-) GENSENSE TECHNOLOGIES INC.

XX PA  
XX PT  
XX DR  
XX XX  
XX Wright JA, Young AH, Dugoud D;  
WPI: 2001.355633/37.  
PT Novel antisense compounds targeting nucleic acid encoding gI or  
gII genes of microorganism, which hybridize with and inhibit  
expression of the genes, useful to inhibit growth of microorganism  
having the genes -  
PS  
PS Disclosure: Fig 6; 11opp: English.

CC The present invention specifically claims AAH56368 to AAH56832 which are  
CC antisense oligonucleotides to nucleotide sequences encoding gI or  
CC generally, antisense compounds (1) comprising antisense oligonucleotides  
CC of 5-50 bases targeted to a nucleotide sequence encoding gI or gII  
CC shock protein (HSP60) (G), and groES (HSP70) (GS) gene from a  
CC microorganism, where the antisense compound is complementary to gI or  
CC GS of a microorganism and specifically hybridizes with and inhibits the  
CC expression of gI or GS. It is claimed, (1) have antibacterial, antiviral  
CC and antiproliferative activities, and can be used in antisense therapy  
CC and for inhibition of expression of gI or GS in cells or tissues in vitro. (1) are  
CC also useful for inhibiting expression of gI or GS in cells or tissues in vitro. (1) are  
CC also useful for inhibiting the growth of a microorganism, or inhibiting  
CC the expression of gI or GS gene in a microorganism (a bacterial cell or  
CC a virus) having a gI or GS gene which involves administering to the  
CC microorganism or to a cell infected with the microorganism, (1). (1) are  
CC also useful for treating a mammalian pathological condition mediated by  
CC the microorganisms which involves identifying a eukaryotic organism  
CC having a pathological condition mediated by microorganisms having a gI  
CC or GS gene and administering (1) such that the growth of microorganism  
CC is inhibited. The antisense compounds are utilized for diagnostics,  
CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
CC prevent or delay microbial infections in humans. They are also useful as  
CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854  
CC represent PCR primers for groove sequencing which are used in the  
CC exemplification of the present invention. AAH56855 to AAH56870 represent  
CC groove nucleotide sequence given in the present invention.

XX

SO Sequence 2107 BP; 650 A; 400 C; 508 G; 549 T; 0 other;

Query Match 62.4%; Score 1037; DB 22; Length 2107;  
Best Local Similarity 77.5%; Pval. No. 1.2e-261;  
Matches 1250; Conservative 0; Mismatches 365; Indels 0; Gaps

YY 14 TATGGCAAAAGAAATCAAATTTCACAGATGCGGTCTGCCTCATGTGCGCGGAATTGA 73  
DB 484 TATCTCAAAAAGAAATTAATTTTCTCAGATGAGTGCCGTTCCAGCTAATGTGTCGTGTGTGCA 543  
YY 74 TAGTTAGCAGATACCGTCAAGTAAGTAAGTACTGTGTCTTAAAGGGGCCAATGTCTTCTTGA 133  
DB 544 TATCTCTTGACAGTACTGTTAAGTAAGTAAGTCTTGCGGACAAAAGGTCGCATGTCTCTTCTTGA 603  
YY 134 AAAAGCTTTGGTCTCCCTTAATTTACTATATACGCGGGTAACCATCTGTAAAGACATGCA 193  
DB 604 AAAATCATTTGGCTCACACCTTATTTACATACGCGGTGTACATTTGCGCAAGAATAATGA 663  
YY 194 ATTGGAAGATCTTTTGAAGAACATGAGGACAAAATATGTGTCTGGAAGGCGCTCTTAAAC 253  
DB 664 ATTTGAAGACCACTTTTGAAGAAATATGTGGTGCCAATATGTATCGAATGTACTCTTAAAC 723  
YY 254 CAATGATATGTGCTGTATGGGAGCAATCTACTGCAACAGTTTTGACAACACCCTTGTCTCA 313  
DB 724 CAATGATATGCCAGGTGACGGGACTACGACTGCAACAGCTTGGACCCACACTATGTCTCC 783  
YY 314 TGAAGACATAAAAATGTGTACACGAGGTCTTAATCAATTTGGTATCCGTGAGGACATTGA 373  
DB 784 TGAGGATATCAAAAAGCTCACGAGGTGCAAAATCTCAATGTGATATCTGTGTGGGATTGA 843  
YY 374 AATGAGACACCAACGCTTTTGAAGCTTTGAAGAACCATCTGTCAACCTGTATATGTGCA 433  
DB 844 AATGAGACACCAACGCTTTTGAAGCTTTTGAAGAACCATCTGTCAACCTGTATATGTGCA 493



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Query Match	62.48;	Score 1036;	DB 22;	Length 1647;
Best Local Similarity	77.58;	Pred. NO. 2e-261;		
Matches 1255; Conservative	0;	Mismatches 365;	Indels 0;	Gaps 0;

[illegible]

Db	1021	TCGCACCTGTGGGGTATACAAAGTCACCAATCGAAATCAACCTCTGTAATTGACCGT	1080
Oy	1095	GAAGAAATACAAAGACGTTATGGCCGAATTAAGCGGTGGGTAGCTGTATCAAGTAGGA	1154
Db	1081	GAAGAAATTCGAAGACGCTTGGCCAAATGTACGGTGTGTACGGTTATTACGTTGGA	1140
Oy	1155	GGCCCAACAGAGACACTTTAAAGAAATGAACCTGCACATAGAGATGCTCTAAATGCT	1214
Db	1141	GGCCGACACTGAACCTAGTTGAAAAGAAATGAACCTGCACATAGAGATGCTCTAAATGCT	1200
Oy	1215	ACACGTGACGCGCTTGAAGAGATATCGTTGCTGCTGGAGAACACCACTTATTACGTT	1274
Db	1201	ACCTGGGACGCTGTATAAAGATATTGTTGGACGGTGGTGAACACCTCTGGCCATATGG	1260
Oy	1275	ATTGAAAAGTACACACTCTTGACCTTGAAGGGCGATGATCTACTGGACGTATACATTTG	1334
Db	1261	ATTCCAGCGTGTCTACTCTGGAATTTACAGAGATGACAAACAGAGACGTATATTGTT	1320
Oy	1335	CTTCCGTGCTTAAGAAAGCGCTGATCGTCAAAATTCGTTAAATCGTGGTAGAAGGCTCC	1394
Db	1321	CTCTCGCTTTGGAAAGAACCGCTTCGTCAAAATTCGTCACATCGAAGATTGAAGGATCT	1380
Oy	1395	GTGATTTATATGCAAGTTGAAAACAGCGCTCGAAGAACAGATTTAATGCTGCACAGGT	1454
Db	1381	ATCGTTATCGAGTGGTTGAAAATATCGAGCGTTGTATAGGATTTACAGCAAGACTGCG	1440
Oy	1455	GAGTGGGTGATTTGATTTAAACAGGAATCATTTGACCCGTCAAGTAAACAGATACGG	1514
Db	1441	GAGTGGGTAACTATGATTTACAGAGATCATTTGATTCGATTTAAATAGCGCTTAGCG	1500
Oy	1515	CTTCAAAATGACCTCTGTACGTACGTATATTTGACACAGAAAGCGTTGTTCTTAAT	1574
Db	1501	CTCAAAATGACACTCTGTATGACGAGCTTGATTTGACAAAGAAAGCGTGTGAGCAAT	1560
Oy	1575	AAACTGACCCAGCTACGCCACGGCCACGAATGCCACAGATGTGATTCAGGAATGATG	1634
Db	1561	AAACGAGACCACTATACCCCAAGCTCCACAGGAATGATGCCAAGTATGATGGGGGGAATGAG	1620

RESULT 13
AAV52210
ID AAV52210 standard; DNA; 5365 BP.
XX
AC AAV52210;
DT 23-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae genome fragment SEQ ID NO:77.
XX
KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KX computer readable medium; vaccine; pharmaceutical composition; ds.
XX
OS Streptococcus pneumoniae.
PN
PN MO9818931-42.
PD
PD 07-MAY-1998.
XX
XX 30-OCT-1997; 97MO-US19588.
XX
XX 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
PI Kunsch CA, Rosen CA;
XX
DR WPI; 1998-272225/24.
XX
XX Computer-readable medium with recorded Streptococcus pneumoniae
PI polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT

PT pneumonae  
 XX  
 XS Claim 1: Page 628-631: 1409pp: English.

CC The present invention describes a computer readable medium which has  
 CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)  
 CC recorded on it, or a representative fragment or a sequence at least 95%  
 CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in  
 CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from  
 CC *Streptococcus pneumoniae*. The present invention also describes an  
 CC isolated nucleic acid molecule encoding a homologue of any of the  
 CC fragments of the *S. pneumoniae* genome (SEQ ID NO:1 to 391) where the  
 CC nucleic acid molecule is produced by a process comprising: (a) screening  
 CC a genomic DNA library using as a probe a target sequence defined by any  
 CC of the sequences in SEQ ID NO:1 to 391, identifying members of the  
 CC library which contain sequences that hybridize to the target sequence and  
 CC isolating the nucleic acid molecules from the members; or (b) isolating  
 CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid  
 CC molecules whose nucleotide sequence is homologous to amplification  
 CC primers derived from the fragment of the *S. pneumoniae* genome to prime  
 CC the amplification and isolating the amplified sequences. The computer  
 CC readable medium can be used in a computer-based system for identifying  
 CC fragments of the *S. pneumoniae* genome of commercial importance, or  
 CC expression modulating fragments of the *S. pneumoniae* genome. Products  
 CC from the present invention can be used in diagnosis kits and assays, and  
 CC pharmaceutical compositions and vaccines for *S. pneumoniae*.

Sequence 5365 BP; 1654 A; 960 C; 1082 G; 1669 T; 0 other:

Query Match 62.3% Score 1035.4; DB 19; Length 5365;  
 Best Local Similarity 77.4%; Pred. No. 4,66-261;  
 Matches 1255; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

OY 14 TATGCAAAAGAAATCAATTTTCAGACATGCGGTGCTGCGCATGTCGCGAGATTGA 73  
 DB 277 TATGCAAAAGAAATCAATTTTCAGACATGCGGTGCTGCGCATGTCGCGAGATTGA 336  
 OY 74 TATGCAAGACATACCGTCAAAAGTACCGTCTTAAGAGGCGCAATGTTGTTCTGA 133  
 DB 337 TATGCAAGACATACCGTCAAAAGTACCGTCTTAAGAGGCGCAATGTTGTTCTGA 396  
 OY 134 AAAAGCTTTGGTCTCCCTTAATTAATGACGGGTGTAACCATGCTTAAGAGATCA 193  
 DB 397 AAAAGCTTTGGTCTCCCTTAATTAATGACGGGTGTAACCATGCTTAAGAGATCA 456  
 OY 194 ATTAGAAGATCATTGTAAGAACATGAGCAAAATGCTGCTGAAGTGGCTTTAAAC 253  
 DB 457 ATTAGAAGATCATTGTAAGAACATGAGCAAAATGCTGCTGAAGTGGCTTTAAAC 516  
 OY 254 CATGATATTGCTGATGATGAGGAGACTCTGCAACAGTTTGAACAGCAATGTTCA 313  
 DB 517 CATGATATTGCTGATGATGAGGAGACTCTGCAACAGTTTGAACAGCAATGTTCA 576  
 OY 314 TGAAGCACTAAAAATGTGACAGAGGTCTTAATCAATTTGATTCCTGAGGATGA 373  
 DB 577 TGAAGCACTAAAAATGTGACAGAGGTCTTAATCAATTTGATTCCTGAGGATGA 636  
 OY 374 AACAGCAACGCAACAGCTGTTGAAGCCATTGCTCAACTGTATGTCGCA 433  
 DB 637 AACAGCAACGCAACAGCTGTTGAAGCCATTGCTCAACTGTATGTCGCA 696  
 OY 434 GGAAGCTATTGCTGAGTCTGCTGATATCATACGCTGTAAGAAAGTTGAGAGTAT 493  
 DB 697 GGAAGCTATTGCTGAGTCTGCTGATATCATACGCTGTAAGAAAGTTGAGAGTAT 756  
 OY 494 CTCACAACTATTGAGCGGTGGGCAAGATGATGTTTACATCGAAGAACTGAGAG 553  
 DB 757 CTCACAACTATTGAGCGGTGGGCAAGATGATGTTTACATCGAAGAACTGAGAG 816  
 OY 554 TATGAAAGAAAGAACTGAAAGTGGTGAAGCAATTTGAGCGGTGTTACTGCTCA 613  
 DB 817 TATGAAAGAAAGAACTGAAAGTGGTGAAGCAATTTGAGCGGTGTTACTGCTCA 876

OY 614 ATACATGTCACAGACAAATGAAAAATGCTGACAGACTTGAAGAACCCATTATCTAT 673  
 DB 877 GTACATGTCACAGACAAATGAAAAATGCTGACAGACTTGAAGAACCCATTATCTAT 936  
 OY 674 CACGATAAAAAGTGTCAAAATCCAAAGACATTTGGCCACTACTGAGAACTCTTAA 733  
 DB 937 TACGACAAAGAAATTTCCAAATTCGAAAGAAATTTGGCCACTACTGAGAACTCTTAA 996  
 OY 734 AACCAACGCTTCATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 793  
 DB 997 AACCAACGCTTCATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1056  
 OY 794 TGTCTTGAACAAGATTCGTGATGATGATGATGATGATGATGATGATGATGATGAT 853  
 DB 1057 TGTCTTGAACAAGATTCGTGATGATGATGATGATGATGATGATGATGATGATGAT 1116  
 OY 854 TGATCTGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 913  
 DB 1117 TGACCTGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176  
 OY 914 AGAGATCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 973  
 DB 1177 AGAGATCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1236  
 OY 974 GATTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033  
 DB 1237 GATTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1296  
 OY 1034 TGCTAACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1093  
 DB 1297 TGCTAACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1356  
 OY 1094 TGAAGAACTGACAAAGCTTTGCGAAATTAAGTGGTGTGATGATGATGATGATGAT 1153  
 DB 1357 TGAAGAACTGACAAAGCTTTGCGAAATTAAGTGGTGTGATGATGATGATGATGAT 1416  
 OY 1154 AGCTCCAGACAGACAGCTTTAAAGAAATGCAATGAGATGATGATGATGATGATGATGAT 1213  
 DB 1417 AGCTCCAGACAGACAGCTTTAAAGAAATGCAATGAGATGATGATGATGATGATGATGAT 1476  
 OY 1214 TACAGCTGAGCGCTTGAAGAAAGTATGATGATGATGATGATGATGATGATGATGAT 1273  
 DB 1477 TACAGCTGAGCGCTTGAAGAAAGTATGATGATGATGATGATGATGATGATGATGAT 1336  
 OY 1274 TATTGAAAGATGACAGCTTGTGAGCTGATGAGGCGATGATGATGATGATGATGATGAT 1333  
 DB 1537 TATTGAAAGATGACAGCTTGTGAGCTGATGAGGCGATGATGATGATGATGATGATGAT 1396  
 OY 1334 GCTTCGCTGCTTAAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGAT 1393  
 DB 1537 TCTCGCTGCTGCTTAAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGAT 1556  
 OY 1394 GGTATGATGACAGGTTGAAAGACAGCCCTGAGGACAGGATTTAATGCTGCAACAG 1453  
 DB 1657 GGTATGATGACAGGTTGAAAGACAGCCCTGAGGACAGGATTTAATGCTGCAACAG 1516  
 OY 1454 TGAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1513  
 DB 1717 TGAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1776  
 OY 1514 GCTTCAAAATGACCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1573  
 DB 1777 GCTTCAAAATGACCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1636  
 OY 1574 TAAACCTGACACCTGACAGGCGGACGACGATGATGATGATGATGATGATGATGATGAT 1633  
 DB 1837 TAAACCTGACACCTGACAGGCGGACGACGATGATGATGATGATGATGATGATGATGAT 1896  
 OY 1634 G 1634  
 DB 1897 G 1897





Db 1698 TGAATAATTCAGAACGCTTGCCAAATTCAGTGTGACGGTTATTAAGTTGC 1757  
 OY 1154 ACCTCAACAGACAGACGCTTTAAAGAAATTCGATTTGAGTGTCTAAATGC 1213  
 Db 1758 ACCCCCACTGAAACTGAGTTGAAAGAAATGAACTCCGATTTGAAGTCCCTCAAGC 1817  
 OY 1214 TACAGTGCAGCGCTTGAAGAAAGTATCGTGTGGTGGAGACAGACTTATACGT 1273  
 Db 1818 TACTGTGCAGCTGTTGAAGAAAGTATTTCTGCAGGTGTGGAGACAGCTTCCAAATG 1877  
 OY 1274 TATGAAAAAGTAGCAGCTCTGAGCTTGAAGGAGATGCTACTAGCAGTAACCTGT 1333  
 Db 1878 GATTCACGCTGAAGCTACTGGAATTCGACGAGATGAGACAGAGAGCTAATATGT 1937  
 OY 1334 GCTTCGCTCTTGAAGAGCTGTAGCTCAATTCCTTAAATGCTGGTACAGAGCTC 1393  
 Db 1938 TCTCCGCTTTGGAGAACCCGCTGCTAAATGCTCAACAAAGCAGATTTAAGATC 1997  
 OY 1394 CGTAGTTATGACAGTTGAAAAACAGCCCTGACAGAGAGATTTAATCTGCAACAG 1453  
 Db 1998 TATGTTATGATCGTTTGAATAATCTGAGCTGTATAGATTTAAACGCAACATCG 2057  
 OY 1454 TGAAGTGGTTGATATGATTTAAACAGAGATGATGACCTGTCAAGTAACAGATCAGC 1513  
 Db 2058 CGAGTGGTAAACATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2117  
 OY 1514 GCTTCAAAATGACAGCTTCTGAGCTAGTGTATTTGAGACAGAGAGATTTGCTAA 1573  
 Db 2118 CCTCAAAATGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2177  
 OY 1574 TAAAGCTGAACAGCTAGCAGCGGACGCAATCCGAGAGTATGATGATGATGATGAT 1633  
 Db 2178 TAAACGAAACGATGAGCCCACTGACAGCAATGATGATGATGATGATGATGATGAT 2237  
 OY 1634 G 1634  
 Db 2238 G 2238  
 RESULT 15  
 ID ABA90521 standard: DNA: 2365589 BP.  
 AC ABA90521:  
 DT 16-MAY-2002 (first entry)  
 DE Genomic sequence of *Lactococcus lactis* IL1403.  
 KM Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.  
 OS *Lactococcus lactis* IL1403.  
 PN FR2807446-A1.  
 PD 12-OCT-2001.  
 PF 11-APR-2000; 2000FR-0004630.  
 PR 11-APR-2000; 2000FR-0004630.  
 PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 PI Boletine A, Sorokine A, Renault P, Ehrlich SD:  
 PT WPI; 2002-04318/06.  
 PS New nucleotide sequence useful in the identification of *Lactococcus*  
 PS Lactis and related species.  
 CC Claim 1: SEQ ID 1: 2504bp; French.  
 CC The present invention is related to a *Lactococcus lactis* nucleotide

CC sequence (ABA90521) and related proteins (AB53300-AB55621). The  
 CC nucleic acid sequence is useful in the detection and/or amplification of  
 CC nucleic acid sequence, particularly to identify *Lactococcus lactis* or  
 CC related species. The proteins of the invention are useful for the  
 CC biosynthesis or biodegradation of a composition of interest. The  
 CC invention helps research in lactic bacteria, particularly useful in the  
 CC production of yogurt and cheese.  
 CC Note: The sequence data for this patent is based on equivalent patent  
 CC WO200177334 (published 18-OCT-2001) which is available in electronic  
 CC format directly from WIPO at [http://wipo.int/pub/published\\_pat\\_sequences](http://wipo.int/pub/published_pat_sequences).  
 XX  
 SO Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;  
 Query Match 57.58; Score 955; DB 24; Length 2365589;  
 Best Local Similarity 75.18; Pred. No. 6.4e-239;  
 Matches 1192; Conservative 0; Mismatches 395; Indels 0; Gaps 0;  
 OY 11 TCATATGCAAAAGAAATCAATTTTCAGACATGCGGTGCTGCCATGTTGGCGGAGT 70  
 Db 398893 TAAATGCAAAAGAAATCAATTTTCAGATGCTGAGAACAGCATGATGCTGGAT 398952  
 OY 71 TCATATGTTGACGATACCGTCAAGTAACGCTGTCTAAAGGCCATGTCTTCT 130  
 Db 398953 TCATATGTTGCTGATACGATGTAACACCTGTGACAAAAGTCCATGTTGTTCT 399012  
 OY 131 TGAAGAGCTTTGGTCTCTCTTAATTCATATGACGGGTACCATTTGCTAAAGAT 190  
 Db 399013 TGAAGAGCTTTGGTCTCTCTTAATTCATATGACGGGTACCATTTGCTAAAGAT 399072  
 OY 191 GCAATTAAGATCATTTTGAACATATGAGACAAAATTTGTGTCTGAAGTGGCTCTAA 250  
 Db 399073 TGAATTAAGATCATTTTGAACATATGAGACAAAATTTGTGTCTGAAGTGGCTCTAA 399132  
 OY 251 AACCAATGATATTTGTTGATGAGGACGACTGCAACAGTTTGAACACAGCATTTGT 310  
 Db 399133 AACCAATGATATTTGTTGATGAGGACGACTGCAACAGCATTTGTGACACAGCATTTGT 399192  
 OY 311 TCATGAGGACATAAAATGTAACAGAGTCTATCAATTTGATTCGTGAGAGCAT 370  
 Db 399193 TCATGAGGACATAAAATGTAACAGAGTCTATCAATTTGATTCGTGAGAGCAT 399252  
 OY 371 TGAAGAGCAACAGCAGCTGTGAAGCCATTTGCAACGCTGATCTGATCTGAG 430  
 Db 399253 TGAAGAGCAACAGCAGCTGTGAAGCCATTTGCAACGCTGATCTGATCTGATCTGAG 399312  
 OY 431 CAGAGAGCTATGCTGAGTGCCTGATCATCATCATCATCATCATCATCATCATCATCAT 490  
 Db 399313 TAAATGCAATTTGCGCAAGTAGTACGTTTCATCATCATCATCATCATCATCATCAT 399372  
 OY 491 TATCTCAGAGCTATGAGCGTGTGCGCAACGATGTGTGATTTACATCGAAGATCTCG 550  
 Db 399373 TATTTCTGATGCAATGAGCGTGTGCGCAACGATGTGTGATTTACATCGAAGATCTCG 399432  
 OY 551 AGCATATGAAAGAGACTTGAAGTGGTGAAGCATGCAATTTGACCGTGTACTGTC 610  
 Db 399433 AGCATATGAAAGAGACTTGAAGTGGTGAAGCATGCAATTTGACCGTGTACTGTC 399492  
 OY 611 TCAATACATGCTACAGCAATGAAAAATGTTGCGAGACTTGAAGAAACCATTTATCT 670  
 Db 399493 TCAATACATGCTTCTAATACAGAAAAATGTTGCGAGACTTGAAGAAACCATTTATCT 399552  
 OY 671 AATACGAGAAAAAAGTGTCAACATGCAAGACATTTGCGACTGATGAGAGTCT 730  
 Db 399553 TATTAACGAGAAAAAAGTGTCTAATACAGAAAAATTTTACGCTGTGAAGAAATCTT 399612  
 OY 731 TAAACCAACGCTCATTTACTCATTTTTCAGATGATGAGTGTGAGAACCTTCAAC 790  
 Db 399613 GAAACCAACGCTCATTTACTCATTTTTCAGATGATGAGTGTGAGAACCTTCAAC 399672  
 OY 791 CTTTGTCTGAACAGATTTGCTACTTCAATGTGTGCTGTCAACGCGCAGAT 850  
 Db 399673 CTTTGTCTTAATTAAGATTAAGTGTCTCAATGTGTGCTGTCAACGCGCAGAT 399732

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OY	851	TGCTGTCGTCGTAAGCGTATCGCTTAAGACATTCGTAACTTTCACAGCGTGTACAGTGTAT	910
Db	399733	TGCTGTCGTCGTAAGCGTATTCGAATTCGAGAAATTTGGCTACTCTTGACAGCGGTGACAGTAAT	399792
OY	911	TACACAGATCTTGACACTGTAATTTAAAGATGCTACATGACACGCCCTTGACAGCGTGC	970
Db	399793	TACTGAAACACTGGCTGTGATCTCTTAAAGATGCTACTCTTGAACTTTAGACCTTTAGACAAAGAC	399852
OY	971	TGAGATTACAGTTGATTAAGATAGCACAGTAAATTTGTTGAAGTTTCAGAGAGTTACAGAC	1030
Db	399853	TAAAGCAACTGTGTGATTAAGACACACACAACTATGTTGAAGTGTGCTGCTGCTGATGTC	399912
OY	1031	TATTCCTAACCGTATTTGCTACTGTAATTAATCCCAATTAGAAACAACAATCTGCCTTTGA	1090
Db	399913	TATTTCTGATCGGTAGCTATTTATTAAGCGCAAAATTTGAAAAACAATCTGATTTTGA	399972
OY	1091	CCGTAAACAACTACAAAGAGTTTGGCAAAATTAGCTGTGTGTAGCTGTATCAAACT	1150
Db	399973	TGCTGAAAAATTTACAAAGAGCTTGTGCAAAATTAGCTGTGTGTGTGCAGTGTGTAAAT	400032
OY	1151	AGACACTTCACACAGAGACCTTTAAAGAAATGAACCTTGATGAGATGAGATGCTTAA	1210
Db	400033	TGCTGTGTGCAACGTAAGACAGCTCAAGCATTAAGCATCTGTGATTAAGATGACACTTA	400092
OY	1211	TGCTACACGTGACGCGCTGTAAAGAGATTCGTGTGTGTGTGTAACAGCACTATTAC	1270
Db	400093	TGCACACGTGACGCGCTGTAGAGAGATTTGTTGTGTGTGTGTGTGTGTGTGTAA	400152
OY	1271	GCTTTTGAAGAAAGTACGACCTCTTGACCTTGAAGGCGATGACTACGTGACGTAACT	1330
Db	400153	TGCTATTGCTGCTTGGATTAACCTTTCAGAAAGAGAAATTTCAACAGGTATTTAACT	400212
OY	1331	TCTGCTTGTGCTGTAGAGAGCCTGTACGTCAAAATTCCTTTAAATGCTGTGATACAAAG	1390
Db	400213	TCTTGCGCGGTGCTGTGAAMACAGTTCGTCAAAATTCGTGCCAATGACGATATTAAG	400272
OY	1391	CTCGGTGATTATGACAACTTGAANAACACCCCTGCAGGAACAGATTTAATCTCTCAAC	1450
Db	400273	TTCAATATCATATTGATAAATTCGTTCAGAAAGAAAGTAAAGTACAGATTCATTCCTCAAC	400332
OY	1451	ACGTGATGTGGTGTGATATGATTTAAACAGGAATCTTACCTGTCACAAAGTAACAGACT	1510
Db	400333	TGTCATATGGGTAAATATGATTAAGAAAGAAATGTGTACCCGTCAAAAGTAATCTCTTC	400392
OY	1511	ACCGCTCAAAATGACCTTCGTGTAGCATCTTTTGTGAACAACGAAGACTGTTC	1570
Db	400393	ACCTTTCAAAACGGGGCTCTGTGTGCTGGTTAATTTTGTACTACTGAAGAGTAAATGTC	400452
OY	1571	TAAATAACTGACACTTACCCGAC	1597
Db	400453	TAAATAACTGACACTTACCCGAC	400479

Search completed: April 15, 2003, 01:18:55  
Job time : 3259.59 secs